

Cathy H Wu

List of Publications by Year in descending order

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207
papers

39,349
citations

26630

56
h-index

5255

165
g-index

222
all docs

222
docs citations

222
times ranked

54785
citing authors

#	ARTICLE	IF	CITATIONS
1	UniProt: the universal protein knowledgebase in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D480-D489.	14.5	4,709
2	UniProt: a hub for protein information. <i>Nucleic Acids Research</i> , 2015, 43, D204-D212.	14.5	4,370
3	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004, 32, 115D-119.	14.5	2,994
4	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	14.5	2,743
5	The Gene Ontology resource: enriching a GOld mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
6	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	14.5	1,712
7	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2004, 33, D154-D159.	14.5	1,681
8	The InterPro protein families and domains database: 20 years on. <i>Nucleic Acids Research</i> , 2021, 49, D344-D354.	14.5	1,385
9	InterPro in 2017â€”beyond protein family and domain annotations. <i>Nucleic Acids Research</i> , 2017, 45, D190-D199.	14.5	1,358
10	UniRef clusters: a comprehensive and scalable alternative for improving sequence similarity searches. <i>Bioinformatics</i> , 2015, 31, 926-932.	4.1	1,223
11	The InterPro protein families database: the classification resource after 15 years. <i>Nucleic Acids Research</i> , 2015, 43, D213-D221.	14.5	1,205
12	Reorganizing the protein space at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2012, 40, D71-D75.	14.5	1,196
13	Activities at the Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2014, 42, D191-D198.	14.5	1,162
14	UniRef: comprehensive and non-redundant UniProt reference clusters. <i>Bioinformatics</i> , 2007, 23, 1282-1288.	4.1	1,144
15	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006, 34, D187-D191.	14.5	961
16	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	14.5	921
17	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	14.5	478
18	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	14.5	444

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19	The Protein Information Resource. <i>Nucleic Acids Research</i> , 2003, 31, 345-347.	14.5	385
20	The Human Proteome Project: Current State and Future Direction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009993.	3.8	294
21	Accomplishments and challenges in literature data mining for biology. <i>Bioinformatics</i> , 2002, 18, 1553-1561.	4.1	229
22	Protein sequence databases. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 76-80.	6.1	201
23	Software for pre-processing Illumina next-generation sequencing short read sequences. <i>Source Code for Biology and Medicine</i> , 2014, 9, 8.	1.7	196
24	PIRSF: family classification system at the Protein Information Resource. <i>Nucleic Acids Research</i> , 2004, 32, 112D-114.	14.5	193
25	The Protein Information Resource: an integrated public resource of functional annotation of proteins. <i>Nucleic Acids Research</i> , 2002, 30, 35-37.	14.5	186
26	Proteomic and Bioinformatic Characterization of the Biogenesis and Function of Melanosomes. <i>Journal of Proteome Research</i> , 2006, 5, 3135-3144.	3.7	183
27	The Protein Information Resource (PIR). <i>Nucleic Acids Research</i> , 2000, 28, 41-44.	14.5	165
28	Protein Bioinformatics Databases and Resources. <i>Methods in Molecular Biology</i> , 2017, 1558, 3-39.	0.9	154
29	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1999, 27, 39-43.	14.5	149
30	Text mining for the biocuration workflow. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas020-bas020.	3.0	132
31	BioC: a minimalist approach to interoperability for biomedical text processing. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat064-bat064.	3.0	123
32	iPTMnet: an integrated resource for protein post-translational modification network discovery. <i>Nucleic Acids Research</i> , 2018, 46, D542-D550.	14.5	120
33	Protein classification artificial neural system. <i>Protein Science</i> , 1992, 1, 667-677.	7.6	112
34	Oncogenic fusion protein EWS-FLI1 is a network hub that regulates alternative splicing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1307-16.	7.1	109
35	BioThesaurus: a web-based thesaurus of protein and gene names. <i>Bioinformatics</i> , 2006, 22, 103-105.	4.1	106
36	Prediction of catalytic residues using Support Vector Machine with selected protein sequence and structural properties. <i>BMC Bioinformatics</i> , 2006, 7, 312.	2.6	105

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37	Protein family classification and functional annotation. <i>Computational Biology and Chemistry</i> , 2003, 27, 37-47.	2.3	103
38	The Protein Ontology: a structured representation of protein forms and complexes. <i>Nucleic Acids Research</i> , 2011, 39, D539-D545.	14.5	102
39	A fast Peptide Match service for UniProt Knowledgebase. <i>Bioinformatics</i> , 2013, 29, 2808-2809.	4.1	101
40	Artificial neural networks for molecular sequence analysis. <i>Computers & Chemistry</i> , 1997, 21, 237-256.	1.2	95
41	Representative Proteomes: A Stable, Scalable and Unbiased Proteome Set for Sequence Analysis and Functional Annotation. <i>PLoS ONE</i> , 2011, 6, e18910.	2.5	94
42	Overview of the BioCreative III Workshop. <i>BMC Bioinformatics</i> , 2011, 12, S1.	2.6	88
43	The iProClass integrated database for protein functional analysis. <i>Computational Biology and Chemistry</i> , 2004, 28, 87-96.	2.3	86
44	New techniques for extracting features from protein sequences. <i>IBM Systems Journal</i> , 2001, 40, 426-441.	3.0	80
45	Framework for a Protein Ontology. <i>BMC Bioinformatics</i> , 2007, 8, S1.	2.6	78
46	Molecular Mechanisms Mediating the Effect of Mono-(2-Ethylhexyl) Phthalate on Hormone-Stimulated Steroidogenesis in MA-10 Mouse Tumor Leydig Cells. <i>Endocrinology</i> , 2010, 151, 3348-3362.	2.8	78
47	Neural networks for full-scale protein sequence classification: Sequence encoding with singular value decomposition. <i>Machine Learning</i> , 1995, 21, 177-193.	5.4	77
48	A crowdsourcing open platform for literature curation in UniProt. <i>PLoS Biology</i> , 2021, 19, e3001464.	5.6	74
49	Protein Ontology (PRO): enhancing and scaling up the representation of protein entities. <i>Nucleic Acids Research</i> , 2017, 45, D339-D346.	14.5	73
50	Protein Information Resource: a community resource for expert annotation of protein data. <i>Nucleic Acids Research</i> , 2001, 29, 29-32.	14.5	72
51	A comprehensive protein-centric ID mapping service for molecular data integration. <i>Bioinformatics</i> , 2011, 27, 1190-1191.	4.1	70
52	An overview of the BioCreative 2012 Workshop Track III: interactive text mining task. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bas056-bas056.	3.0	68
53	BioCreative III interactive task: an overview. <i>BMC Bioinformatics</i> , 2011, 12, S4.	2.6	65
54	Transcription factors and genetic circuits orchestrating the complex, multilayered response of <i>Clostridium acetobutylicum</i> to butanol and butyrate stress. <i>BMC Systems Biology</i> , 2013, 7, 120.	3.0	65

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55	Dependence network modeling for biomarker identification. <i>Bioinformatics</i> , 2007, 23, 198-206.	4.1	64
56	Protein Ontology: a controlled structured network of protein entities. <i>Nucleic Acids Research</i> , 2014, 42, D415-D421.	14.5	63
57	SkateBase, an elasmobranch genome project and collection of molecular resources for chondrichthyan fishes. <i>F1000Research</i> , 2014, 3, 191.	1.6	61
58	Elevated FGF21 secretion, PGC-1 β and ketogenic enzyme expression are hallmarks of iron-sulfur cluster depletion in human skeletal muscle. <i>Human Molecular Genetics</i> , 2014, 23, 24-39.	2.9	59
59	TnCentral: a Prokaryotic Transposable Element Database and Web Portal for Transposon Analysis. <i>MBio</i> , 2021, 12, e0206021.	4.1	56
60	BioTagger-GM: A Gene/Protein Name Recognition System. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2009, 16, 247-255.	4.4	54
61	Structural and functional studies of S-adenosyl-L-methionine binding proteins: a ligand-centric approach. <i>BMC Structural Biology</i> , 2013, 13, 6.	2.3	50
62	miRTex: A Text Mining System for miRNA-Gene Relation Extraction. <i>PLoS Computational Biology</i> , 2015, 11, e1004391.	3.2	50
63	Comparative bioinformatics analyses and profiling of lysosome-related organelle proteomes. <i>International Journal of Mass Spectrometry</i> , 2007, 259, 147-160.	1.5	49
64	RNA-Seq Analysis of Abdominal Fat in Genetically Fat and Lean Chickens Highlights a Divergence in Expression of Genes Controlling Adiposity, Hemostasis, and Lipid Metabolism. <i>PLoS ONE</i> , 2015, 10, e0139549.	2.5	49
65	Back-propagation and counter-propagation neural networks for phylogenetic classification of ribosomal RNA sequences. <i>Nucleic Acids Research</i> , 1994, 22, 4291-4299.	14.5	46
66	BioCreative-IV virtual issue. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau039-bau039.	3.0	43
67	Plant Protein Annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , 2005, 138, 59-66.	4.8	42
68	Omics-Based Molecular Target and Biomarker Identification. <i>Methods in Molecular Biology</i> , 2011, 719, 547-571.	0.9	42
69	RLIMS-P 2.0: A Generalizable Rule-Based Information Extraction System for Literature Mining of Protein Phosphorylation Information. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 17-29.	3.0	42
70	iProClass: an integrated database of protein family, function and structure information. <i>Nucleic Acids Research</i> , 2003, 31, 390-392.	14.5	41
71	Prediction of residue-residue contact matrix for protein-protein interaction with Fisher score features and deep learning. <i>Methods</i> , 2016, 110, 97-105.	3.8	41
72	iProLINK: an integrated protein resource for literature mining. <i>Computational Biology and Chemistry</i> , 2004, 28, 409-416.	2.3	40

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73	Alterations in the Global Proteome and Phosphoproteome in Third Generation EGFR TKI Resistance Reveal Drug Targets to Circumvent Resistance. <i>Cancer Research</i> , 2021, 81, 3051-3066.	0.9	38
74	Overview of the interactive task in BioCreative V. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw119.	3.0	36
75	DynGO: a tool for visualizing and mining of Gene Ontology and its associations. <i>BMC Bioinformatics</i> , 2005, 6, 201.	2.6	35
76	PIRSF Family Classification System for Protein Functional and Evolutionary Analysis. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	1.2	35
77	Quantitative Assessment of Dictionary-based Protein Named Entity Tagging. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2006, 13, 497-507.	4.4	35
78	PIRSF family classification system for protein functional and evolutionary analysis. <i>Evolutionary Bioinformatics</i> , 2007, 2, 197-209.	1.2	35
79	Computational analysis and identification of amino acid sites in dengue E proteins relevant to development of diagnostics and vaccines. <i>Virus Genes</i> , 2007, 35, 175-186.	1.6	34
80	iProClass: an integrated, comprehensive and annotated protein classification database. <i>Nucleic Acids Research</i> , 2001, 29, 52-54.	14.5	32
81	Integrative annotation and knowledge discovery of kinase post-translational modifications and cancer-associated mutations through federated protein ontologies and resources. <i>Scientific Reports</i> , 2018, 8, 6518.	3.3	31
82	Integration of bioinformatics resources for functional analysis of gene expression and proteomic data. <i>Frontiers in Bioscience - Landmark</i> , 2007, 12, 5071.	3.0	30
83	UniProt genomic mapping for deciphering functional effects of missense variants. <i>Human Mutation</i> , 2019, 40, 694-705.	2.5	29
84	Phylogenomic Analysis of Marine Roseobacters. <i>PLoS ONE</i> , 2010, 5, e11604.	2.5	29
85	ProClass Protein Family Database. <i>Nucleic Acids Research</i> , 1999, 27, 272-274.	14.5	28
86	BioCreative V BioC track overview: collaborative biocurator assistant task for BioGRID. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw121.	3.0	28
87	Proteomic Analysis of Pathways Involved in Estrogen-Induced Growth and Apoptosis of Breast Cancer Cells. <i>PLoS ONE</i> , 2011, 6, e20410.	2.5	28
88	Protein Bioinformatics Databases and Resources. <i>Methods in Molecular Biology</i> , 2011, 694, 3-24.	0.9	27
89	Gene and Protein Profiling of the Response of MA α 10 Leydig Tumor Cells to Human Chorionic Gonadotropin. <i>Journal of Andrology</i> , 2004, 25, 900-913.	2.0	26
90	Tunable synthetic extracellular matrices to investigate breast cancer response to biophysical and biochemical cues. <i>APL Bioengineering</i> , 2019, 3, 016101.	6.2	26

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91	iPTMnet: Integrative Bioinformatics for Studying PTM Networks. <i>Methods in Molecular Biology</i> , 2017, 1558, 333-353.	0.9	26
92	Update on genome completion and annotations: Protein Information Resource. <i>Human Genomics</i> , 2004, 1, 229.	2.9	25
93	A comparison study on algorithms of detecting long forms for short forms in biomedical text. <i>BMC Bioinformatics</i> , 2007, 8, S5.	2.6	25
94	Transcriptional profiling of liver during the critical embryo-to-hatchling transition period in the chicken (<i>Gallus gallus</i>). <i>BMC Genomics</i> , 2018, 19, 695.	2.8	25
95	RLIMS-P: an online text-mining tool for literature-based extraction of protein phosphorylation information. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau081-bau081.	3.0	23
96	Construction of phosphorylation interaction networks by text mining of full-length articles using the eFIP system. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	3.0	23
97	[5] Gene classification artificial neural system. <i>Methods in Enzymology</i> , 1996, 266, 71-88.	1.0	22
98	iTextMine: integrated text-mining system for large-scale knowledge extraction from the literature. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	22
99	Community annotation in biology. <i>Biology Direct</i> , 2010, 5, 12.	4.6	21
100	iSimp: A sentence simplification system for biomedical text. , 2012, , .		21
101	Coordination between TGF- β 2 cellular signaling and epigenetic regulation during epithelial to mesenchymal transition. <i>Epigenetics and Chromatin</i> , 2019, 12, 11.	3.9	21
102	Substring selection for biomedical document classification. <i>Bioinformatics</i> , 2006, 22, 2136-2142.	4.1	20
103	The eFIP system for text mining of protein interaction networks of phosphorylated proteins. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas044-bas044.	3.0	20
104	A generalizable NLP framework for fast development of pattern-based biomedical relation extraction systems. <i>BMC Bioinformatics</i> , 2014, 15, 285.	2.6	20
105	Integrated Bioinformatics for Radiation-Induced Pathway Analysis from Proteomics and Microarray Data. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 047-060.	0.4	20
106	Protein Bioinformatics Infrastructure for the Integration and Analysis of Multiple High-Throughput Proteomics Data. <i>Advances in Bioinformatics</i> , 2010, 2010, 1-19.	5.7	19
107	BioCreative-2012 Virtual Issue. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas049-bas049.	3.0	19
108	Classification neural networks for rapid sequence annotation and automated database organization. <i>Computers & Chemistry</i> , 1993, 17, 219-227.	1.2	18

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109	ProClass protein family database. <i>Nucleic Acids Research</i> , 2000, 28, 273-276.	14.5	18
110	Systems Integration of Biodefense Omics Data for Analysis of Pathogen-Host Interactions and Identification of Potential Targets. <i>PLoS ONE</i> , 2009, 4, e7162.	2.5	18
111	piNET: a versatile web platform for downstream analysis and visualization of proteomics data. <i>Nucleic Acids Research</i> , 2020, 48, W85-W93.	14.5	18
112	BIO-AJAX. <i>SIGMOD Record</i> , 2004, 33, 51-57.	1.2	17
113	Using distant supervision to augment manually annotated data for relation extraction. <i>PLoS ONE</i> , 2019, 14, e0216913.	2.5	17
114	Understanding ER+ Breast Cancer Dormancy Using Bioinspired Synthetic Matrices for Long-Term 3D Culture and Insights into Late Recurrence. <i>Advanced Biology</i> , 2020, 4, e2000119.	3.0	17
115	COVID-19 Knowledge Graph from semantic integration of biomedical literature and databases. <i>Bioinformatics</i> , 2021, 37, 4597-4598.	4.1	17
116	Motif identification neural design for rapid and sensitive protein family search. <i>Bioinformatics</i> , 1996, 12, 109-118.	4.1	16
117	Computational identification of strain-, species- and genus-specific proteins. <i>BMC Bioinformatics</i> , 2005, 6, 279.	2.6	16
118	Sequence signatures in envelope protein may determine whether flaviviruses produce hemorrhagic or encephalitic syndromes. <i>Virus Genes</i> , 2009, 39, 1-9.	1.6	16
119	Document classification for mining host pathogen protein-protein interactions. <i>Artificial Intelligence in Medicine</i> , 2010, 49, 155-160.	6.5	16
120	A framework for biomedical figure segmentation towards image-based document retrieval. <i>BMC Systems Biology</i> , 2013, 7, S8.	3.0	16
121	Evolutionary Model Selection and Parameter Estimation for Protein-Protein Interaction Network Based on Differential Evolution Algorithm. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 622-631.	3.0	16
122	miRiaD: A Text Mining Tool for Detecting Associations of microRNAs with Diseases. <i>Journal of Biomedical Semantics</i> , 2016, 7, 9.	1.6	16
123	Automatic gene annotation using GO terms from cellular component domain. <i>BMC Medical Informatics and Decision Making</i> , 2018, 18, 119.	3.0	16
124	Completing sparse and disconnected protein-protein network by deep learning. <i>BMC Bioinformatics</i> , 2018, 19, 103.	2.6	16
125	An extended dependency graph for relation extraction in biomedical texts. , 2015, , .		16
126	Protein Name Tagging Guidelines: Lessons Learned. <i>Comparative and Functional Genomics</i> , 2005, 6, 72-76.	2.0	15

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127	Construction of protein phosphorylation networks by data mining, text mining and ontology integration: analysis of the spindle checkpoint. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat038.	3.0	15
128	Prediction of contact matrix for protein-protein interaction. Bioinformatics, 2013, 29, 1018-1025.	4.1	15
129	BioC interoperability track overview. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau053-bau053.	3.0	15
130	A Protein Class Database Organized with ProSite Protein Groups and PIR Superfamilies. Journal of Computational Biology, 1996, 3, 547-561.	1.6	14
131	The representation of protein complexes in the Protein Ontology (PRO). BMC Bioinformatics, 2011, 12, 371.	2.6	14
132	eGARD: Extracting associations between genomic anomalies and drug responses from text. PLoS ONE, 2017, 12, e0189663.	2.5	14
133	Neural networks for molecular sequence classification. Mathematics and Computers in Simulation, 1995, 40, 23-33.	4.4	13
134	Inference of protein-protein interaction networks from multiple heterogeneous data. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 8.	1.4	13
135	Title is missing!. Applied Intelligence, 1997, 7, 27-38.	5.3	12
136	Challenges and Solutions in Proteomics. Current Genomics, 2007, 8, 21-28.	1.6	12
137	pGenN, a Gene Normalization Tool for Plant Genes and Proteins in Scientific Literature. PLoS ONE, 2015, 10, e0135305.	2.5	12
138	Bioinformatics Knowledge Map for Analysis of Beta-Catenin Function in Cancer. PLoS ONE, 2015, 10, e0141773.	2.5	12
139	Evolutionary analysis and interaction prediction for protein-protein interaction network in geometric space. PLoS ONE, 2017, 12, e0183495.	2.5	12
140	Noise Reduction Methods for Distantly Supervised Biomedical Relation Extraction. , 2017, , .		12
141	Predicting Ligand Binding Residues and Functional Sites Using Multipositional Correlations with Graph Theoretic Clustering and Kernel CCA. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 992-1001.	3.0	11
142	DEXTER: Disease-Expression Relation Extraction from Text. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	11
143	Artificial neural system for gene classification using a domain database. , 1990, , .		10
144	Integrative Computational and Experimental Approaches to Establish a Post-Myocardial Infarction Knowledge Map. PLoS Computational Biology, 2014, 10, e1003472.	3.2	10

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145	Characterization of metabolic responses, genetic variations, and microsatellite instability in ammonia-stressed CHO cells grown in fed-batch cultures. <i>BMC Biotechnology</i> , 2021, 21, 4.	3.3	10
146	eFIP: A Tool for Mining Functional Impact of Phosphorylation from Literature. <i>Methods in Molecular Biology</i> , 2011, 694, 63-75.	0.9	10
147	TGF-beta signaling proteins and the Protein Ontology. <i>BMC Bioinformatics</i> , 2009, 10, S3.	2.6	9
148	An Automatic System for Extracting Figures and Captions in Biomedical PDF Documents. , 2011, , .		9
149	iSimp in BioC standard format: enhancing the interoperability of a sentence simplification system. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau038-bau038.	3.0	9
150	An Integrated Approach for Analyzing Clinical Genomic Variant Data from Next-Generation Sequencing. <i>Journal of Biomolecular Techniques</i> , 2015, 26, 19-28.	1.5	9
151	Protein ontology on the semantic web for knowledge discovery. <i>Scientific Data</i> , 2020, 7, 337.	5.3	9
152	Protein classification using a neural network database system. , 1991, , .		8
153	Use of the Protein Ontology for Multi-Faceted Analysis of Biological Processes: A Case Study of the Spindle Checkpoint. <i>Frontiers in Genetics</i> , 2013, 4, 62.	2.3	7
154	Pattern Discovery for Wide-Window Open Information Extraction in Biomedical Literature. , 2018, , .		7
155	Analysis of Protein Phosphorylation and Its Functional Impact on Protein-Protein Interactions via Text Mining of the Scientific Literature. <i>Methods in Molecular Biology</i> , 2017, 1558, 213-232.	0.9	7
156	Structure-Guided Rule-Based Annotation of Protein Functional Sites in UniProt Knowledgebase. <i>Methods in Molecular Biology</i> , 2011, 694, 91-105.	0.9	7
157	Document Classification for Mining Host Pathogen Protein-Protein Interactions. , 2008, , .		6
158	Robust segmentation of biomedical figures for image-based document retrieval. , 2012, , .		6
159	BioC-compatible full-text passage detection for protein-protein interactions using extended dependency graph. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw072.	3.0	6
160	eGenPub, a text mining system for extending computationally mapped bibliography for UniProt Knowledgebase by capturing centrality. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	3.0	6
161	PIRSitePredict for protein functional site prediction using position-specific rules. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	5
162	Using an artificial neural system to determine the knowledge based of an expert system. , 1990, , .		4

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163	Neural networks for molecular sequence database management. , 1991, , .		4
164	Mapping Gene/Protein Names in Free Text to Biomedical Databases. , 2007, , .		4
165	ngsShoRT. , 2013, , .		4
166	PENNER: Pattern-enhanced Nested Named Entity Recognition in Biomedical Literature. , 2018, , .		4
167	Global analysis of switchgrass (<i>Panicum virgatum</i> L.) transcriptomes in response to interactive effects of drought and heat stresses. <i>BMC Plant Biology</i> , 2022, 22, 107.	3.6	4
168	CANS: an interactive neural network system for CRAY supercomputers. , 1992, , .		3
169	GENE FAMILY IDENTIFICATION NETWORK DESIGN FOR PROTEIN SEQUENCE ANALYSIS. <i>International Journal on Artificial Intelligence Tools</i> , 1999, 08, 419-432.	1.0	3
170	Building a classifier for identifying sentences pertaining to disease-drug relationships in tardive dyskinesia. , 2012, , .		3
171	Protein-protein interaction network inference from multiple kernels with optimization based on random walk by linear programming. , 2015, , .		3
172	Protein-protein interaction prediction based on multiple kernels and partial network with linear programming. <i>BMC Systems Biology</i> , 2016, 10, .	3.0	3
173	Computational clustering for viral reference proteomes: Table 1.. <i>Bioinformatics</i> , 2016, 32, 2041-2043.	4.1	3
174	Protein-Centric Data Integration for Functional Analysis of Comparative Proteomics Data. <i>Methods in Molecular Biology</i> , 2011, 694, 323-339.	0.9	3
175	Neural Networks for Molecular Sequence Classification. , 1994, , 279-305.		3
176	Title is missing!. <i>Machine Learning</i> , 1995, 21, 177-193.	5.4	2
177	A comparison study of biomedical short form definition detection algorithms. , 2006, , .		2
178	iProLINK: A Framework for Linking Text Mining with Ontology and Systems Biology. , 2008, , .		2
179	Predicting ligand binding residues using multi-positional correlations and kernel canonical correlation analysis. , 2010, , .		2
180	Pathway curation: Application of text-mining tools eGIFT and RLIMS-P. , 2012, , .		2

#	ARTICLE	IF	CITATIONS
181	Toll-Like Receptor Signaling in Vertebrates: Testing the Integration of Protein, Complex, and Pathway Data in the Protein Ontology Framework. PLoS ONE, 2015, 10, e0122978.	2.5	2
182	Development of Bioinformatics Pipeline for Analyzing Clinical Pediatric NGS Data. AMIA Summits on Translational Science Proceedings, 2015, 2015, 207-11.	0.4	2
183	Framework for a protein ontology. , 2006, , .		1
184	Protein bioinformatics. , 2008, , 203-222.		1
185	Studying Biocuration Workflows. Nature Precedings, 2009, , .	0.1	1
186	An Image-Text Approach for Extracting Experimental Evidence of Protein-Protein Interactions in the Biomedical Literature. , 2013, , .		1
187	Text Mining of Protein Phosphorylation Information Using a Generalizable Rule-Based Approach. , 2013, , .		1
188	Docking features for predicting binding loss due to protein mutation. , 2014, , .		1
189	Enhancing interacting residue prediction with integrated contact matrix prediction in protein-protein interaction. Eurasip Journal on Bioinformatics and Systems Biology, 2016, 2016, 17.	1.4	1
190	Predicting nsSNPs that Disrupt Protein-Protein Interactions Using Docking. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1082-1093.	3.0	1
191	A FAMILY CLASSIFICATION APPROACH TO FUNCTIONAL ANNOTATION OF PROTEINS. , 2004, , 417-434.		1
192	PROTEIN CLASSIFICATION ARTIFICIAL NEURAL SYSTEM: A FILTER PROGRAM FOR DATABASE SEARCH. , 1993, , .		0
193	Annotation of Protein Sequences. , 0, , 131-147.		0
194	The PIR SuperFamily (PIRSF) classification system. , 2005, , .		0
195	Biocuration Workflow Catalogue. Nature Precedings, 2009, , .	0.1	0
196	Predicting functional sites in biological sequences using canonical correlation analysis. , 2009, , .		0
197	Mining impact of protein modifications on protein-protein interactions from literature. , 2009, , .		0
198	Prediction of Catalytic Residues in Proteins Using a Consensus of Prediction (CoP) Approach. , 2010, , .		0

#	ARTICLE	IF	CITATIONS
199	DDI2PPI. , 2014, , .		0
200	Cloud-based Semantic Integration and Knowledge Discovery Systems in Precision Medicine. , 2018, , .		0
201	RESTful API for iPTMnet. , 2018, , .		0
202	The PIR for Functional Genomics and Proteomics. , 2003, , 431-442.		0
203	The Protein Information Resource for Functional Genomics and Proteomics. , 2003, , 117-137.		0
204	Dynamically generating a protein entity dictionary using online resources. , 2005, , .		0
205	Protein Complex Mention Recognition with Web-Based Knowledge Learning. Lecture Notes in Computer Science, 2018, , 190-197.	1.3	0
206	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	0
207	Scalable Text Mining Assisted Curation of Post-Translationally Modified Proteoforms in the Protein Ontology. CEUR Workshop Proceedings, 2016, 1747, .	2.3	0